

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Lal, Preeti
Shah, Purvi
Corley, Neil C.

(ii) TITLE OF THE INVENTION: HUMAN PREPRONEUROTENSIN/NEUROMEDIN N

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0450 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PITUNOT03
(B) CLONE: 1760566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Met Ala Gly Met Lys Ile Gln Leu Val Cys Met Leu Leu Leu Ala
 1 5 10 15
 Phe Ser Ser Trp Ser Leu Cys Ser Asp Ser Glu Glu Glu Met Lys Ala
 20 25 30
 Leu Glu Ala Asp Phe Leu Thr Asn Met His Thr Ser Lys Ile Ser Lys
 35 40 45
 Ala His Val Pro Ser Trp Lys Met Thr Leu Leu Asn Val Cys Ser Leu
 50 55 60
 Val Asn Asn Leu Asn Ser Pro Ala Glu Glu Thr Gly Glu Val His Glu
 65 70 75 80
 Glu Glu Leu Val Ala Arg Arg Lys Leu Pro Thr Ala Leu Asp Gly Phe
 85 90 95
 Ser Leu Glu Ala Met Leu Thr Ile Tyr Gln Leu His Lys Ile Cys His
 100 105 110
 Ser Arg Ala Phe Gln His Trp Glu Leu Ile Gln Glu Asp Ile Leu Asp
 115 120 125
 Thr Gly Asn Asp Lys Asn Gly Lys Glu Glu Val Ile Lys Arg Lys Ile
 130 135 140
 Pro Tyr Ile Leu Lys Arg Gln Leu Tyr Glu Asn Lys Pro Arg Arg Pro
 145 150 155 160
 Tyr Ile Leu Lys Arg Asp Ser Tyr Tyr Tyr
 165 170

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

NNTCAAAGCC	AGCTGAAGGA	AAGAGGAAGT	GCTAGAGAGA	GCCCCCTTC	GTGTGCTTCT	60
GA	ACTTTTACG	GA	CTTGCTT	GTAGAAGGC	TGAAAGATGA	120
CTTGATGCA	TGCTACTCCT	GGCTTCAGC	TCCTGGAGTC	TGTGCTCAGA	TTCAGAAGAG	180
GAAATGAAAG	CATTAGAAC	AGATTTCTTG	ACCAATATGC	ATACATCAA	GATTAGTAAA	240
GCACATGTT	CCTCTGGAA	GATGACTCTG	CTAAATGTT	GCAGTCTTGT	AAATAATTG	300
AACAGCCCAG	CTGAGGAAAC	AGGAGAAGTT	CATGAAGAGG	AGCTTGTG	AAGAAGGAAA	360
CTTCCTACTG	CTTAGATGG	CTTAGCTTG	GAAGCAATGT	TGACAATATA	CCAGCTCCAC	420
AAAATCTGTC	ACAGCAGGGC	TTTCAACAC	TGGGAGTTAA	TCCAGGAAGA	TATTCTTGAT	480
ACTGGAAATG	ACAAAAATGG	AAAGGAAGAA	GTCATAAAGA	GAAAAATTCC	TTATATTCTG	540
AAACGGCAGC	TGTATGAGAA	AAAACCCAGA	AGACCCTACA	TACTCAAAG	AGATTCTTAC	600
TATTACTGAG	AGAATAAAATC	ATTATTTAC	ATGTGATTGT	GATTCATCAT	CCCTTAATTA	660
AATATCAAAT	TATATTGTG	TGAAAATGTG	ACAAACACAC	TTATCTGTCT	CTTCTACAAAT	720
TGTGGTTTAT	TGAATGTGAT	TTTCTGCAC	TAATATAAT	TAGACTAAGT	GTTTCAAAT	780
AAATCTAAAT	CTTCAGCATG	ATGTGTTGTG	TATAATTGGA	GTAGATATTA	ATTAAGTCAC	840
CTGTATAATG	TTTGTAATT	TTGCAAAACA	TATCTTGAGT	TGTTTAAACA	GTCAAATGT	900
TTGATATT	ATACCAGCTT	ATGAGCTCAA	AGTACTACAG	CAAAGCCTAG	CCTGCATATC	960
ATTCA	AACAAAGTAA	TAGCGCCTCT	TTTATTATTT	TGACTGAATG	TTTTATGGAA	1020
TTGAAAGAAA	CATACGTTCT	TTTCAAGACT	TCCTCATGAA	TCTCTCAATT	ATAGGAAAAG	1080
TTATTGTGAT	AAAATAGGAA	CAGCTGAAAG	ATTGATTAAT	GAACTATTGT	TATTACTTCC	1140
TATTAAATG	AATGACATTG	AACTGGATT	TTTGACCTGT	TAATGGACTT	GGTAGCTATT	1200
AGAAGGACAC	TTGACCTCCA	ATAGAAAAAA	AATAAGAAA	TAAAAGAAG	TATAAAAGTA	1260
ATAAAATAAA	ATCAGAAGAG	AAAAAGAAA	AGAAAAGTAA	AAAGAGGGGG	GACACACCAT	1320
AAGAACCAAT	ACCCGGGAAT	TTCGGAGCG	A			1351

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 163424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ala Gly Met Lys Ile Gln Leu Val Cys Met Ile Leu Leu Ala Phe
1 5 10 15
Ser Ser Trp Ser Leu Cys Ser Asp Ser Glu Glu Glu Met Lys Ala Leu
20 25 30
Glu Thr Asp Leu Leu Thr Asn Met His Thr Ser Lys Ile Ser Lys Ala
35 40 45
Ser Val Pro Ser Trp Lys Met Ser Leu Leu Asn Val Cys Ser Leu Ile
50 55 60
Asn Asn Leu Asn Ser Gln Ala Glu Glu Thr Gly Glu Phe His Glu Glu
65 70 75 80
Glu Leu Ile Thr Arg Arg Lys Phe Pro Ala Ala Leu Asp Gly Phe Ser
85 90 95
Leu Glu Ala Met Leu Thr Ile Tyr Gln Leu Gln Lys Ile Cys His Ser
100 105 110
Arg Ala Phe Gln His Trp Glu Leu Ile Gln Glu Asp Ile Leu Asp Ala
115 120 125
Gly Asn Asp Lys Asn Glu Lys Glu Glu Val Ile Lys Arg Lys Ile Pro
130 135 140
Tyr Ile Leu Lys Arg Gln Leu Tyr Glu Asn Lys Pro Arg Arg Pro Tyr
145 150 155 160
Ile Leu Lys Arg Gly Ser Tyr Tyr Tyr
165

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 92546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ile Gly Met Asn Leu Gln Leu Val Cys Leu Thr Leu Leu Ala Phe
1 5 10 15
Ser Ser Trp Ser Leu Cys Ser Asp Ser Glu Glu Asp Val Arg Ala Leu
20 25 30
Glu Ala Asp Leu Leu Thr Asn Met His Ala Ser Lys Val Ser Lys Gly
35 40 45
Ser Pro Pro Ser Trp Lys Met Thr Leu Leu Asn Val Cys Ser Leu Ile
50 55 60
Asn Asn Leu Asn Ser Ala Ala Glu Glu Ala Gly Glu Met Arg Asp Asp
65 70 75 80
Asp Leu Val Ala Lys Arg Lys Leu Pro Leu Val Leu Asp Asp Phe Ser
85 90 95

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Leu Glu Ala Leu Leu Thr Val Phe Gln Leu Gln Lys Ile Cys Arg Ser
100 105 110
Arg Ala Phe Gln His Trp Glu Ile Ile Gln Glu Asp Ile Leu Asp His
115 120 125
Gly Asn Glu Lys Thr Glu Lys Glu Glu Val Ile Lys Arg Lys Ile Pro
130 135 140
Tyr Ile Leu Lys Arg Gln Leu Tyr Glu Asn Lys Pro Arg Arg Pro Tyr
145 150 155 160
Ile Leu Lys Arg Ala Ser Tyr Tyr Tyr
165